SEQUENCE LISTING

<110> Japan Science and Technology Corporation
      manager of Natinal Insutitute of Infectious Diseases

<120> Medicine for promoting ceramide transportation, sequence for
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Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
            35                  40                  45


Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
    50                  55                  60


Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65                  70                  75                  80


Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
                85                  90                  95


Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
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Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
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Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
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Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145   150   155   160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
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Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
        180   185   190

Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
        195   200   205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
    210   215   220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225   230   235   240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
            245   250   255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
        260   265   270

Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
        275   280   285

Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe

Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305   310   315   320

Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
            325   330   335

Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
            340   345   350

Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
            355   360   365

Gln Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln
            370   375   380

Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu
385   390   395   400

Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp
            405   410   415

Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val
            420   425   430

Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr
            435   440   445

Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile
       450   455   460

Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val
465   470   475   480

Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp

Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala
            500   505   510

Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile
            515   520   525

Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg
            530   535   540

Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly
545   550   555   560

Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr
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Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala
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Gly Lys Pro Ile Leu Phe
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            20   25   30

Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
            35   40   45

Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
    50   55   60

Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65   70   75   80

Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
                85   90   95

Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
            100   105   110

Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
        115   120   125

Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
    130   135   140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145   150   155   160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
            165   170   175

Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
            180   185   190

Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
        195   200   205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
    210   215   220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225   230   235   240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
                    245   250   255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
            260   265   270

Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
        275   280   285

Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe
    290   295   300

Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305   310   315   320

Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
            325   330   335

Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
            340   345   350

Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
        355   360   365

Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val
    370   375   380

Ser Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met
385   390   395   400

Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala
            405   410   415

Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
        420   425   430

Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
435   440   445

Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn
450   455   460

Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
465   470   475   480

Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys
485   490   495

Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile
500   505   510

Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val
515   520   525

Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys
530   535   540

Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
545   550   555   560

Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys
565   570   575

Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
580   585   590

Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg
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Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
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Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
        35   40   45

Asn Asn Thr Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
    50   55   60

Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65   70   75   80

Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
            85   90   95

Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
            100   105   110

Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
        115   120   125

Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
    130   135   140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
    145   150   155   160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
                165   170   175

Thr Leu Gln Lys Tyr Phe Asp Val Cys Ala Asp Ala Val Ser Lys Asp
                180   185   190

Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
            195   200   205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Asn Thr Asn Gly Asn Lys
    210   215   220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225   230   235   240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
                245   250   255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Glu Ser
            260   265   270

Trp Gln Lys Arg His Asp Lys Glu Met Glu Lys Arg Arg Arg Leu Glu
        275   280   285

Glu Ala Tyr Lys Asn Ala Met Ala Glu Leu Lys Lys Lys Pro Arg Phe
    290   295   300

Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305   310   315   320

Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
                325   330   335

Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Pro
            340   345   350

Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
      355   360   365

Gln Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln
     370   375   380

Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu
385   390   395   400

Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp
          405   410   415

Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val
         420   425   430

Cys Asn Tyr Phe Trp Ser Val Asp Val Arg Asn Asp Trp Glu Thr Thr
      435   440   445

Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile
     450   455   460

Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val
465   470   475   480

Leu Tyr Leu Ser Ala Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp
         485   490   495

Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala
        500   505   510

Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile
        515   520   525

Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg
     530   535   540

Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly
545   550   555   560

Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr
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Pro Lys Phe Leu Lys Arg Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala
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Gly Lys Pro Ile Leu Phe
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Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
                35   40   45

Asn Asn Thr Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
        50   55   60

Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
65   70   75   80

Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
                85   90   95

Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
          100   105   110

Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
          115   120   125

Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
          130   135   140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145   150   155   160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
              165   170   175

Thr Leu Gln Lys Tyr Phe Asp Val Cys Ala Asp Ala Val Ser Lys Asp
          180   185   190

Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
          195   200   205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Asn Thr Asn Gly Asn Lys
210   215   220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225   230   235   240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
              245   250   255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Glu Ser
          260   265   270

Trp Gln Lys Arg His Asp Lys Glu Met Glu Lys Arg Arg Arg Leu Glu
          275   280   285

Glu Ala Tyr Lys Asn Ala Met Ala Glu Leu Lys Lys Lys Pro Arg Phe
290   295   300

Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305   310   315   320

Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
325   330   335

Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Pro
340   345   350

Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
355   360   365

Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val
370   375   380

Ser Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met
385   390   395   400

Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala
405   410   415

Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
420   425   430

Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
435   440   445

Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Ser
450   455   460

Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
465   470   475   480

Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys
485 490 495

Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Ala Ile
500 505 510

Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val
515 520 525

Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys
530 535 540

Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
545 550 555 560

Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys
565 570 575

Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
580 585 590

Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg
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atgccttttc ttctgttggg acccatagat ttgtacaaaa ggttgaagag atggtacaga
1560

accacatgac ttactcatta caggatgtag gtggtgatgc gaattggcaa ctagttgtag
1620

aagaaggaga aatgaaggta tacagaagag aagtcgaaga aaatggaatt gttctggatc
1680

ctttgaaagc tacccatgca gttaaaggtg ttacaggaca cgaagtctgc aattactttt
1740

ggagtgttga tgttcgcaat gactgggaaa ctactataga aaacttccat gtagtggaaa
1800

cattagctga taatgcaatc atcatttatc aaacgcacaa gagagtgtgg cctgcttctc
1860

agagagatgt actgtatctt tctgctattc gaaagatccc agccttgact gagaacgacc

1920

ctgagacttg gatagtttgt aatttttctg tggatcatga cagcgctcct ctgaacaatc
1980

gatgtgtccg tgccaaaatc aatgttgcta tgatttgtca aaccttagta agcccaccag
2040

agggaaacca ggaaataagc agagacaaca ttctgtgcaa gattacatat gtagctaatg
2100

tgaacccagg aggatgggca ccagcctcgg tgttaagagc agtggcaaaa cgagaatatc
2160

ctaaatttct aaaacgtttt acttcttacg tccaagaaaa aactgcagga aaaccaattt
2220

tgttttagta tgtacagtga ctgaagcaag gctgtgtgac attccatgtt ggagaaagaa
2280

agaagaaaaa ttgagttctc taagctggaa cataggatct acagccttgt ccatggccca
2340

agaagaatca ttgcaatagt aaagctgggt atctaacact agccatctcc tgatagatct
2400

ccttgctcaa tgtgtaacta taaatacatg taaaatcaca tgcaaaaaaa aaaaaaaaa
2460

aaaaaaaaaa aaa
2473

<210> 8
<211> 1872
<212> DNA
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<400> 8
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120

caggatcgtt gggtagtttt gaaaaataat actttgagtt actacaaatc tgaagatgag
180

21/30

acagagtacg gttgcagggg atccatctgt cttagcaagg ctgtgatcac acctcatgat
240

tttgatgaat gtcggtttga tatcagtgtt aatgatagtg tttggtatct tcgtgctcag
300

gacccagatc acagacagca gtggatagat gccattgaac agcacaagac tgaatcagga
360

tatggatctg agtccagctt acgtagacat ggctcaatgg tgtcactggt gtctggagca
420

agtgggtact ctgctacatc cacatcttca ttcaagaaag gacacagttt acgtgagaaa
480

ttggctgaaa tggaaacttt tagagacatc ttatgtagac aagttgacac tctccaaaag
540

tactttgatg tctgtgctga tgctgtctcc aaggatgaac ttcaaaggga taaagtggta
600

gaagatgatg aagatgactt ccctacaact cgttctgatg gagacttttt gcacaatacc
660

aatggtaata aggaaaaatt atttccacat gtaaccccca aaggaattaa tggtatagac
720

tttaaagggg aagcaataac ttttaaagca actactgctg gaatccttgc tacactttct
780

cattgtattg aattaatggt aaaacgggaa gagagctggc aaaaaagaca tgataaggaa
840

atggagaaga aagacgatt agaggaagca tacaagaatg caatggcaga gcttaagaag
900

aaaccccgtt ttggagggcc tgattatgaa gaaggtccga acagtctgat taatgaggag
960

gagttctttg atgctgttga agctgctctt gacagacaag ataaaataga ggaacagtca
1020

cagagcgaga aggtcaggtt acactggcct acacctttgc catctggaga tgccttttct
1080

tctgttggga cccatagatt tgtacaaaag ccctatagtc gctcttcctc catgtcttcc
1140

22／30

attgatctag tcagtgcctc tgacgatgtt cacagattca gctcccaggt tgaagagatg
1200

gtacagaacc acatgactta ctcattacag gatgtaggtg gtgatgcgaa ttggcaacta
1260

gttgtagaag aaggagaaat gaaggtatac agaagagaag tcgaagaaaa tggaattgtt
1320

ctggatcctt tgaaagctac ccatgcagtt aaaggtgtta caggacacga agtctgcaat
1380

tacttttgga gtgttgatgt tcgcaatgac tgggaaacta ctatagaaaa cttccatgta
1440

gtggaaacat tagctgataa tgcaatcatc atttatcaaa cgcacaagag agtgtggcct
1500

gcttctcaga gagatgtact gtatctttct gctattcgaa agatcccagc cttgactgag
1560

aacgaccctg agacttggat agtttgtaat ttttctgtgg atcatgacag cgctcctctg
1620

aacaatcgat gtgtccgtgc caaaatcaat gttgctatga tttgtcaaac cttagtaagc
1680

ccaccagagg gaaaccagga aataagcaga gacaacattc tgtgcaagat tacatatgta
1740

gctaatgtga acccaggagg atgggcacca gcctcggtgt taagagcagt ggcaaaacga
1800

gaatatccta aatttctaaa acgttttact tcttacgtcc aagaaaaaac tgcaggaaaa
1860

ccaattttgt tt
1872

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

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    22

<210> 10
<211> 27
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<220>
<223> PCR primer

<400> 10
cttaagctag cttgccaaac ctacagg
    27

<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 11
cagaattcac catgtcggat aatcagagct gg
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<210> 12
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<212> DNA
<213> Artificial Sequence

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<223> PCR primer

<400> 12
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    56

<210> 13
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 13
ggctcgagct agaacaaaat aggctttcct gc
     32

<210> 14
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 14
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     53

<210> 15
<211> 75
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<213> Artificial Sequence

<220>
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<400> 15
cagaggcact gactagatca atggaagaca tggaggaaga gcgactatag ggcttttgga
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caaatctatg tgtcc
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<210> 16
<211> 72
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<213> Artificial Sequence

<220>
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<400> 16
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60
tggtgcagaa cc
  72

<210> 17
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<210> 18
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<400> 18
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<210> 19
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<210> 20
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<400> 20
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<210> 21
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<400> 21
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<210> 22
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<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 22
ggctcgagct aagatctagt cttgtgctgt tcaatggc
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<210> 23
<211> 35
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<220>
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<400> 23
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<210> 24
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<212> DNA
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<220>
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<400> 24
ggctcgagct aagatctttg gacaaatcta tgtgtccc
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<210> 25
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     32

<210> 26
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gagaaagtgt agcaaggatt ccagcagtag ttgc
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<400> 29
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<210> 30
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<400> 30
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    27

<210> 31
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<212> DNA
<213> Artificial Sequence

<220>
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<400>   31
aagatcccag ccttgactg
    19

<210>   32
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<212>   DNA
<213>   Artificial Sequence

<220>
<223>   PCR primer

<400>   32
ggctcgagga acaaaatagg ctttcctgc
    29